AMENDMENTS TO THE CLAIMS

A detailed listing of all claims that are, or were, in the present application, irrespective of whether the claim(s) remains under examination in the application are presented below. The claims are presented in ascending order and each includes one status identifier.

1. (Original) A method for determining the presence of neoplastic molecular markers in a host comprising:

a) obtaining a test sample from the host;

b) identifying the presence of neoplastic molecular markers in the test sample using an array of neoplastic molecular marker specific reagents; and

c) analyzing the array of neoplastic disease molecular marker specific reagents, wherein the analysis yields the identification of a neoplastic disease from which the neoplastic molecular markers originate.

2. (Original) The method of Claim 1, wherein the neoplastic disease is lung cancer.

3. (Original) The method of Claim 1, wherein the neoplastic disease is prostate cancer.

4. (Original) The method of Claim 1, wherein the neoplastic disease is astrocytoma.

5. (Original) The method of Claim 1, wherein the neoplastic disease is neuroblastoma.

6. (Original) The method of Claim 1, wherein the array of neoplastic molecular marker specific reagents is used in an immunological assay method.

7. (Original) The method of Claim 4, wherein the immunological assay method is selected from the group consisting of dot blot analysis, slot blot analysis, and ELISA.

8. (Original) The method of Claim 1, wherein the expression pattern of the array of neoplastic molecular markers is determined by evaluating the quantity of RNA or DNA encoding said markers.

9. (Original) The method of Claim 8, wherein the quantity of RNA or DNA is determined by a method selected from the group consisting of Northern blot analysis, Southern blot analysis, Western blot analysis, RT-PCR, PCR, nucleic acid sequence based amplification assays (NASBA), transcription mediated amplification (TMA), or computerized detection matrix.

10. (Original) An array for identifying a neoplastic source sample, comprising a plurality of neoplastic molecular markers arranged in an assayable format, said molecular markers being differentially expressed as compared to a comparable non-neoplastic source sample.

11. (Original) The array of Claim 10, wherein the array comprises neoplastic molecular marker specific reagents to detect the presence of a small cell lung cancer.

12. (Original) The array of Claim 8, wherein the reagents comprise reagents specific for the detection of NeuroD2, ATH5, Sox 1, Sox2, and LMO4.

13. (Original) The array of Claim 10, wherein the array comprises of neoplastic molecular marker specific reagents to detect the presence of a non-small cell lung cancer.

14. (Original) The array of Claim 13, wherein the reagents comprise reagents specific for the detection of Groucho1, SOX2, SOX3 and NKX5.2.

15. (Original) The array of Claim 13, wherein the reagents comprise reagents specific for the detection of Zic family members.

16. (Original) The array of Claim 15, wherein the reagents comprise reagents specific for the detection of MyT -2, Hes-5, and SMAD6.

17. (Original) The array of Claim 10, wherein the reagents comprise reagents specific for the detection of neuronal genes are selected from the group consisting of Neurogenin-1/MATH4c, Neurogenin-2/MATH4a, Neurogenin-3/MATH4b, Emx-1, Emx-2, Isl1, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, LMO1, LMO2, LMO4, HES1, HES2, HES3, HES4, HES5, HES6, HES7, or combinations thereof.

18. (Original) The array of Claim 10, wherein the reagents comprise reagents specific for HES1, HES2, HES3, HES4, HES5, HES6, HES7, SMAD1, SMAD2, SMAD3, SMAD4, SAMD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10, or combinations thereof.

19. (Original) The array of Claim 10, wherein the reagents comprise reagents specific for HES1, HES2, HES3, HES4, HES5, HES6, HES7, Emx-1, Emx-2, Is11, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, NeuroD 1, NeuroD 2, NeuroD 3, ASH-1/MASH1, ASH-2/MASH2, ASCL-3/reserved, or combinations thereof.

20. (Original) The array of Claim 10, wherein the array comprises neoplastic molecular marker specific reagents indicative of a prostate cancer.

21. (Original) The array of Claim 20, wherein the neoplastic molecular marker specific reagents are indicative of prostate cancer of Group I.

22. (Original) The array of Claim 21, wherein the reagents comprise reagents specific for the detection of NeuroD2, ATH1, Is11, LMO4, and GBX2.

23. (Original) The array of Claim 20, wherein the neoplastic molecular marker specific reagents are indicative of prostate cancer of Group II.

24. (Original) The array of Claim 23, wherein the reagents comprise reagents specific for the detection of Nkx2.2, Sall1, and Sharp 1.

25. (Original) The array of Claim 10, wherein the array comprises neoplastic molecular marker specific reagents are indicative of an astrocytoma.

26. (Original) The array of Claim 25, wherein the neoplastic molecular marker specific reagents are indicative of a subclass I astrocytoma.

27. (Original) The array of Claim 26, wherein the reagents comprise reagents specific for the detection of negative regulators of neural differentiation markers and neuronal genes.

28. (Original) The array of Claim 27, wherein the negative regulators of neural differentiation markers are selected from the group consisting of Msx-1, Msx-2, or combinations thereof.

29. (Original) The array of Claim 27, wherein the neuronal genes are selected from the group consisting of Neurogenin-1/MATH4c, Neurogenin-2/MATH4a, Neurogenin-3/MATH4b, Emx-1, Emx-2, Isl1 Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, LMO1, LMO2, LMO4, HES1, HES2, HES3, HES4, HES5, HES6, HES7, or combinations thereof.

30. (Original) The array of Claim 26, wherein the reagents comprise reagents specific for HES1, HES2, HES3, HES4, HES5, HES6, HES7, SMAD1, SMAD2, SMAD3, SMAD4, SMAD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10, or combinations thereof.

31. (Original) The array of Claim 26, wherein the array comprises high expression of HES genes and neural genes of Neurogenin, NeuroD and ASH family.

32. (Original) The array of Claim 26, wherein the reagents comprise reagents specific for HES1, HES2, HES3, HES4, HES5, HES6, HES7, Emx-1, Emx-2, Is11, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, NeuroD 1, NeuroD 2, NeuroD 3, ASH-1/MASH1, ASH-2/MASH2, ASCL-3/reserved, or combinations thereof.

33. (Original) A method of identifying a treatment for a patient having neoplastic disease comprising:

determining the presence of neoplastic molecular markers in the patient according to the method of Claim 1; and

selecting a therapeutic protocol based upon a correlation between particular therapeutic regimes and the particular markers identified in the determining step.

34. (Original) The method of Claim 33, wherein the presence of one or more neoplastic molecular markers is determined using an immunological assay method.

35. (Original) The method of Claim 34, wherein the immunological assay method is selected from the group consisting of dot blot analysis, slot blot analysis, RIA, peptide microarray, and ELISA.

36. (Original) The method of Claim 33, wherein the presence of one or more neoplastic molecular markers is determined using a molecular biological-based assay methods.

37. (Original) The method of Claim 36, wherein the molecular biological-based assay method is selected from the group consisting of Northern blot analysis, Southern blot analysis, Western blot analysis, RT-PCR, PCR, nucleic acid sequence based amplification assays (NASBA), transcription mediated amplification (TMA), or computerized detection matrix.

38. (Original) The method of Claim 33, wherein the neoplastic molecular markers present are indicative of a small cell lung cancer.

39. (Original) The method of Claim 38, wherein the presence of negative regulators of neural differentiation markers is detected and the presence of neuronal genes is not detected.

40. (Original) The method of Claim 38, wherein the neoplastic molecular markers present are indicative of a small cell lung cancer comprise NeuroD2, ATH5, Sox1, Sox2, and LMO4.

41. (Original) The method of Claim 33, wherein the neoplastic molecular markers present are indicative of a non-small cell lung cancer.

42. (Original) The method of Claim 41, wherein the presence of negative regulators of neural differentiation markers is detected and the presence of neuronal genes is not detected.

43. (Original) The method of Claim 41, wherein the neoplastic molecular markers present are indicative of a non-small cell lung cancer comprise Groucho1, SOX2, SOX3 and NKX5.2.

44. (Original) The method of Claim 33, wherein the neoplastic molecular markers present are indicative of a prostate cancer.

45. (Original) The method of Claim 44, wherein the presence of negative regulators of neural differentiation markers is detected and the presence of neuronal genes is not detected.

46. (Original) The method of Claim 44, wherein the prostate cancer is that of Group I.

47. (Original) The method of Claim 46, wherein the neoplastic molecular markers indicative of prostate cancer of Group I comprise NeuroD2, ATH1, Is11, LMO4, and GBX2.

48. (Original) The method of Claim 44, wherein the neoplastic molecular markers indicative of prostate cancer of Group II.

49. (Original) The method of Claim 48, wherein the neoplastic molecular markers indicative of prostate cancer of Group II comprise Nkx2.2, Sall1, and Sharp1.

50. (Original) The method of Claim 33, wherein the neoplastic molecular markers present are indicative of an astrocytoma.

51. (Original) The method of Claim 50, wherein the astrocytoma is a subclass I astrocytoma.

52. (Original) The method of Claim 51, wherein the presence of negative regulators of neural differentiation markers is detected and the presence of neuronal genes is not detected.

53. (Original) The method of Claim 52, wherein the negative regulators of neural differentiation markers are selected from the group consisting of Msx-1, Msx-2, or combinations thereof.

54. (Original) The method of Claim 52, wherein the neuronal genes not detected are selected from the group consisting of Neurogenin-1/MATH4c, Neurogenin-2/MATH4a, Neurogenin-3/MATH4b, Emx-1, Emx-2, Isl1, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, LMO1, LMO2, LMO4, or combinations thereof.

55. (Original) The method of Claim 52, wherein the negative regulators of neural differentiation markers are selected from the group consisting of SMAD1, SMAD2, SMAD3, SMAD4, SAMD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10, or combinations thereof.

56. (Original) The method of Claim 55, wherein the neuronal genes are selected from the group consisting of NeuroD 1, NeuroD 2, NeuroD 3, ASH-l/MASHl, ASH-2/MASH2, ASCL-3/reserved, or combinations thereof.

57. (Original) The method of Claim 52, wherein the negative regulators of neural differentiation markers are selected from the group consisting of HES1, HES2, HES3, HES4, HES5, HES6, HES7, or combinations thereof.

58. (Original) The method of Claim 57, wherein the neuronal genes are selected from the group consisting of NeuroD 1, NeuroD 2, NeuroD 3, ASH-l/MASH1, ASH-2/MASH2, ASCL-3/reserved, or combinations thereof.

59. (Original) The method of Claim 52, wherein the negative regulators of neural differentiation are selected from the group consisting of HES1, HES2, HES3, HES4, HES5, HES6, HES7, and the neuronal genes are selected from the group consisting of Emx-1, Emx-2, Is11, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, or combinations thereof.

60. (Original) The method of Claim 59, wherein the neuronal genes are selected from the group consisting of NeuroD 1, NeuroD 2, NeuroD 3, ASH-1/MASH1, ASH-2/MASH2, ASCL-3/reserved, or combinations thereof.

61. (Original) The method of Claim 33, wherein the neoplastic molecular markers present are indicative of a neuroblastoma.

62. (Original) The method of Claim 61, wherein the neoplastic molecular markers present are indicative of the neuroblastoma comprise SMAD1, SMAD2, SMAD3, SMAD4, SMAD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10, SHH, Notch1, Notch2, Notch3, Notch4, and TAN-1.

63. (Original) The method of Claim 61, wherein the neoplastic molecular markers present are indicative of the neuroblastoma comprise ASH-1 and Neurogenin1.

64. (Original) The method of Claim 61, wherein the neoplastic molecular markers present are indicative of the neuroblastoma comprise HES5, Hey1, NeuroD1, NeuroD2, and NeuroD3.

65. (Original) A method of treating a neoplastic disease comprising:

providing an assay sample isolated from a subject suspected of having a neoplasm;

determining the presence of one or more neoplastic molecular markers in the sample;

identifying the neoplastic disease from the presence of neoplastic molecular markers determined; and

selecting a therapeutic protocol based upon a correlation between particular therapeutic regimes and particular neoplastic disease states.

66. (Original) The method of Claim 65, wherein the therapeutic regime comprises administering cytokines.

67. (Previously Presented) A method of testing a host for a cancer condition, the method comprising testing a sample obtained from the host for an autoimmune response against a plurality of transcription modulating factors.

68. (Previously Presented) The method of Claim 67, wherein the sample is a tissue or a bodily fluid.

69. (Previously Presented) The method of Claim 67, wherein the sample is a bodily fluid chosen from the group consisting of blood, tears, semen, saliva, serum, and urine.

70. (Previously Presented) The method of Claim 69, wherein testing the sample for the autoimmune response comprises using the sample for an autoantibody against the plurality of transcription modulating factors.

71. (Previously Presented) The method of Claim 67, wherein the at least one transcription modulating factors are immobilized for the testing the sample.

72. (Previously Presented) The method of Claim 71, wherein the testing the sample comprises a dot blot, a slot blot, or an enzyme-linked immunoabsorbent assay.

73. (Previously Presented) The method of Claim 67, wherein the cancer condition is a presence of a cancer cell in the host.

74. (Previously Presented) The method of Claim 73, wherein the cancer cell is an astrocytoma, neuroblastoma or glioblastoma.

75. (Previously Presented) The method of Claim 73, wherein the cancer cell is a lung cancer cell, small cell lung cancer, a non small cell lung cancer, or a prostate cancer cell.

76. (Previously Presented) The method of Claim 67, wherein the sample comprises an NK cell, a T cell, a lymphocyte, or a macrophage

77. (Previously Presented) The method of Claim 67, wherein testing the sample for the autoimmune response comprises detecting the plurality of transcription modulating factors in the sample.

78. (Previously Presented) The method of Claim 77, wherein detecting the plurality of transcription modulating factors in the sample comprises using antibodies against the plurality of transcription modulating factors.

79. (Previously Presented) The method of Claim 77, wherein detecting the plurality of transcription modulating factors in the sample comprises using RT-PCR analysis.

80. (Previously Presented) The method of Claim 77, wherein detecting the plurality of transcription modulating factors in the sample comprises hybridizing a probe to the plurality of transcription modulating factors.

81. (Previously Presented) The method of Claim 67, wherein the host is a human.

82. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors perturbs chromatin structure to permit access of transcriptional components to a gene.

83. (Previously Presented) The method of Claim 82, wherein the at least one transcription modulating factors that perturb chromatin structure to permit access of transcriptional components to a gene are chosen from the group consisting of NURF, CHRAC, ACF, SWI/SNF complex, and SWI/SNF-related (RUSH) proteins.

84. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is involved in the recruitment of a TATA-binding protein (TBP)-containing or not-containing (Initiator) complexes.

85. (Previously Presented) The method of Claim 82, wherein the at least one transcription modulating factors that is involved in the recruitment of a TATA-binding protein (TBP)-containing or not-containing (Initiator) complexes are chosen from the group consisting of TFIIB, TFIID, TFIIE, TFIIF, and TFIII, TRP, and TRF2.

86. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is a TATA-binding protein.

87. (Previously Presented) The method of Claim 67, wherein the TATA binding protein is chosen from the group consisting of a TAFIIA complex, TAFIIAa, TAFIIAb, TAFIIAg, a TAFIIB complex, TAFIIB, RAP74, RAP30, a TAFs forming the TFIID complex, TAFII250, CIF150, TAFII130/135, TAFII100, TAFII70/80, TAFII31/32, TAFII20, TAFII15, TAFII28, TAFII68, TAFII55, TAFII30, TAFII18, TAFII105, a TAFIIE complex, TAFIIEa, TAFIIEb, a

TAFIIF complex, p62, p52, MAT1, p34, XPD/ERCC2, p44, XPB/ERCC3, Cdk7, CyclinH, a RNA polymerase II complex, hRPB1, hRPB2, hRPB3, hRPB4, hRPB5, hRPB6, hRPB7, hRPB8, hRPB9, hRPB10, hRPB11, and hRPB12.

88. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors forms a coactivator complex with TRAP, DRIP, ARC, CRSP, Med, SMCC, or NAT.

89. (Previously Presented) The method of Claim 88, wherein the at least one of the transcription modulating factors forms a coactivator complex with TRAP, DRIP, ARC, CRSP, Med, SMCC, or NAT is chosen from the group consisting of TRAP240/DRIP250, TRAP230/DRIP240, DRIP205/CRSP200/TRIP2/PBP- /RB18A/TRAP220, hRGR1/CRSP150/DRIP150/TRAP170, TRAP150, CRSP130/hSur-2/DRIP130, TIG-1,; CRSP100/TRAP100/DRIP100, DRIP97, DRIP92/TRAP95, CRSP85, CRSP77/DRIP77/TRAP80, CRSP70/DRIP70, Ring3, hSRB10/hCDK8, DRIP36/hMEDp34, CRSP34, CRSP33/hmE7, hMED6, hSRB11/hCyclin C, hSOH1, and hSRB7.

90. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is a protein of the androgen receptor complex.

91. (Previously Presented) The method of Claim 90, wherein the protein of the androgen receptor complex is a member of the group consisting of ANPK, ARIP3, PIAS family, PIASalpha, PIASbeta, PIASgamma, ARIP4.

92. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is a transcriptional co-repressor.

93. (Previously Presented) The method of Claim 92, wherein the transcriptional co-repressor is chosen from the group consisting of N-CoR family, SMRT family, NCOR2/SMRT/TRAC1/CTG26/TNRC14/SMRTE, REA, MSin3, HDAC family, and HDAC5.

94. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of bHLH, suUSF, AP4, E-protein, E2A/E12, E47, HEB/ME1, HEB2/ME2/MITF-2A,B,C/SEF-2/TFE/TF4/R8f, TFE family, TFE3, TFEB, Myc family, Max family, Mad families, and WBSCR14.

95. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of neurogenins, Neurogenin-1/MATH4c, Neurogenin-2/MATH4a, Neurogenin-3/MATH4b, NeuroD, NeuroD-1, NeuroD-2, NeuroD-3(6)/my051/NEX1/MATH2/Dlx-3, NeuroD-4/ATH-3/NeuroM), ATH, ATH-1/MATH1, ATH-5/MATH5, ASH, ASH-1/MASH1, ASH-2/LASH2, ASCL-3/reserved, NSCL, NSCL1/HEN1, NSCL2/HEN2, HAND, Hand1/eHAND/Thing-1, Hand2/dHAND/Thing-2, Mesencephalon-

Olfactory Neuronal bHLHs, COE proteins, COE1, COE2/Olf-1/EBF-LIKE3, COE3/Olf-1, and Homol/Mmot1.

96. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of glia enriched bHLHs, OLIG proteins, Olig1, Olig2/protein kinase C-binding protein RACK17, Olig3, bHLH family of negative regulators, Ids, Id1, Id2, Id3, Id4, DIP1, HES, HES1, HES2, HES3, HES4, HES5, HES6, HES7, SHARP, SHARP1/DEC-2/eip1/Stra13, SHARP2/DEC-1/TR00067497_p, Hey/HRT proteins, Hey1/HRT1/HERP-2/HESR-2, Hey2/HRT2/HERP-1, HRT3, Lyl family, Lyl-1, Lyl-2, RGS family, RGS1, RGSRGS2/G0S8, RGS3/RGP3, capsulin, CENP-B, Mist1; Nhlh1, MOP3, Scleraxis, TCF15, bA305P22.3, and Ipf-1/Pdx-1/Idx-1/Stf-1/Iuf-1/Gsf.

97. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of beta.-catenin, GSK3, Groucho proteins, Groucho-1, Groucho-2, Groucho-3, Groucho-3, TCF family, TCF1A, B, C, D, E, F, G/LEF-1, TCF3, and TCF4, PC4, and MBF1.

98. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of Delta family, Serrate family, Jagged family, Dll1, Dll3, Dll4, Jagged1, Jagged2, Serrate2, Notch family, Notch1, Notch2, Notch3, Notch4, TAN-1, Bearded family, E(spl)m.alpha., E(spl)m2, E(spl)m4, E(spl)m6, Fringe family, Mfng, Rfng, Lfng, Deltex/dx-1, MAML1, RBP-Jk/CBF1/Su(H)/KBF2, and RUNX.

99. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of Chordin, Noggin, Follistatin, SMAD proteins, SMAD1, SMAD2, SMAD3, SMAD4, SAMD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10, SHH, IHH, Su(fu), GLI family, GLI/GLI1, Gli2, Gli3, Zic family, Zic/Zic1, Zic2, and Zic3).

100. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of a Wing helix/forkhead family of transcription factors, BF proteins, BF1, BF-2/Freac4, Fkh5/Foxb1/HFH-e5.1/Mf3, and Fkh6/Freac7.

101. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of HMG transcription factors, Sox proteins, Sox1, Sox2, Sox3, Sox4, Sox6, Sox10, Sox11, Sox13, Sox14 Sox18, Sox21, Sox22, Sox30, HMGIX, HMGIC, HMGIY, and HMG-17.

102. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of Hox proteins, Evx family, Evx1, Evx2, Mox family, Mox1, Mox2, NKL family, NK1, NK3, Nkx3.1, NK4, Lbx family, Lbx1, Lbx2, Tlx family, Tlx1, Tlx2, Tlx3, Emx/Ems family, Emx1, Emx2, Vax family, Vax1, Vax2, Hmx family, Hmx1, Hmx2, Hmx3, NK6 family, Nkx6.1, Msx/Msh family, Msx-1, Msx-2, Cdx, Cdx1, Cdx2,

Xlox family, Lox3, Gsx family, Goosecoid, GSX, GSCL, En family, En-1, En-2, HB9 family, Hb9/HLXB9, Gbx family, Gbx1, Gbx2, Dbx family, Dbx-1, Dbx-2, Dll family, Dlx-1, Dlx-2, Dlx-4, Dlx-5, Dlx-7, Iroquois family, Xiro1, Irx2, Irx3, Irx4, Irx5, Irx6, Nkx, Nkx2.1/TTF-1, Nkx2.2/TTF-2, Nkx2.8, Nkx2.9, Nkx5.1, Nkx5.2, PBC family, Pbx1a, Pbx1b, Pbx2, Pbx3, Prd family, Otx-1, Otx-2, Phox2a, Phox2B, Ptx family, Pitx2, Pitx3/Ptx3, XANF family, Hesx1/XANF-1, BarH family, BarH, Brx2, Cut, and Gtx.

103. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of POU domain factor proteins, Brn2/XlPou2, Brn3a, Brn3b, Brn4/POU3F4, and Brn5/Pou6F1.

104. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of transcription factors with a homeodomain region plus a LIM region, Isl1, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, LMO family, LMO1, LMO2, and LMO4.

105. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of Paired box transcription factors, Pax2, Pax3, Pax5, Pax6, Pax7, and Pax8.

106. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of GATA family, Gata1, Gata2, Gata3,

Gata4/5, Gata6, MyT family, MyT1, MyT1l, MyT2, MyT3, SAL family HSal1, Sal2, Sall3, REST/NRSF/XBR, Snail family, Scratch/Scrt, Zf289, FLJ22251, MOZ, ZFP-38/RU49, Pzf, Mtsh1/teashirt, MTG8/CBF1A-homolog, TIS11D/BRF2/ERF2, TTF-I interacting peptide 21, Znf-HX, Zhx1, KOX1/NGO-St-66, ZFP-15/ZN-15, ZnF20, ZFP200, ZNF/282, HUB1, Finb/RREB1, Nucleai Receptors, liganded, ER family, TR family, RAR familiy, RXR family, PML-RAR family, PML-RXR family, Not1/Nurr, ROR, COUP-TF family, COUP-TF1, and COUP-TF2.

107. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of RING finger transcription factor proteins, KIAA0708, Bfp/ZNF179, BRAP2, KIAA0675, LUN,NSPc1, Neuralized family, neu/Neur-1, Neur-2, Neur-3, Neur-4, RING1A, SSA1/RO52, ZNF173, PIAS family, PIAS-alpha, PIAS-beta, PIAS-gamma, parkin family, and ZNF127 family.

108. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of proteins relating to cell-cycle progression-dedicated components that are part of the RNA polymerase II transcription complex, E2F family, E2F-1, E2F-3, E2F-4, E2F-5, DP family, DP-1, DP-2, p53 family, p53, p63, p73, mdm2; ATM, RB family, RB, p107, and p130.

109. (Previously Presented) The method of Claim 67, wherein at least one of the transcription modulating factors is chosen from the group consisting of factors involved in splicing.

110. (Previously Presented) The method of Claim 67, wherein at least one of the factors involved in splicing is chosen from the group consisting of Hu family, HuA, HuB, HuC, HuD, Musashi1, Nova family, Nova1, Nova2, SR proteins, B1C8, B4A11, ASF SRp20, SRp30, SRp40, SRp55, SRp75, SRm160, SRm300, CC1.3/CC1.4, Def-3/RBM6, SIAHBP/PUF60, Sip1, C1QBP/GC1Q-R/HA13P1/P32, Staufen, TRIP, Zfr, CPSF, and Inducible poly(A)-Binding Protein (U33818).

111. (Previously Presented) A diagnostic device comprising a plurality of reagents that each interact with a chemically distinct antibody against a transcription modulation factor in a sample from a host to produce an independently detectable signal that indicates a presence of the chemically distinct antibody.

112. (Previously Presented) The diagnostic device of Claim 111, comprising at least about ten of the reagents.

113. (Previously Presented) The diagnostic device of Claim 111, comprising at least about twenty of the reagents.

114. (Previously Presented) The diagnostic device of Claim 111, comprising at least about fifty of the reagents.

115. (Previously Presented) The diagnostic device of Claim 111, comprising at least about one hundred of the reagents.

116. (Previously Presented) The diagnostic device of Claim 111, having between about ten and about fifty of the reagents.

117. (Previously Presented) The diagnostic device of Claim 111, wherein the sample is a tissue or a bodily fluid.

118. (Previously Presented) The diagnostic device of Claim 111, wherein the sample is a bodily fluid chosen from the group consisting of blood, tears, semen, saliva, serum, and urine.

119. (Previously Presented) The diagnostic device of Claim 111, wherein the reagents are immobilized for the testing the sample.

120. (Previously Presented) The diagnostic device of Claim 111, comprising the reagents disposed for use in a dot blot, a slot blot, or an enzyme-linked immunoabsorbent assay.

121. (Previously Presented) The diagnostic device of Claim 111, comprising the reagents disposed in a microarray.

122. (Previously Presented) The method of Claim 111, wherein the signal comprises radioactivity, fluorescence, or enzyme activity.

123. (Previously Presented) The diagnostic device of Claim 111, wherein the transcription modulation factors are predictive for astrocytoma, neuroblastoma or glioblastoma.

124. (Previously Presented) The diagnostic device of Claim 111, wherein the transcription modulation factors are predictive for lung cancer, small cell lung cancer, a non small cell lung cancer, or prostate cancer.

125. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of NURF, CHRAC, ACF, SWI/SNF complex, SWI/SNF-related (RUSH) proteins, TFIIB, TFIID, TFIIE, TFIIF, and TFIIH, TRP, TRF2, a TATA-binding protein, a TAFIIA complex, TAFIIAa, TAFIIAb, TAFIIAg, a TAFIIB complex, TAFIIB, RAP74, RAP30, a TAFs forming the TFIID complex, TAFII250, CIF150, TAFII130/135, TAFII100, TAFII70/80, TAFII31/32, TAFII20, TAFII15, TAFII28, TAFII68, TAFII55, TAFII30, TAFII18, TAFII105, a TAFIIE complex, TAFIIEa, TAFIIEb, a TAFIIF complex, p62, p52, MAT1, p34, XPD/ERCC2, p44, XPB/ERCC3, Cdk7, CyclinH, a RNA polymerase II complex, hRPB1, hRPB2, hRPB3, hRPB4, hRPB5, hRPB6, hRPB7, hRPB8, hRPB9, hRPB10, hRPB11, and hRPB12.

126. (Previously Presented) The diagnostic device of Claim 111, wherein at least one of the transcription modulating factors forms a coactivator complex with TRAP, DRIP, ARC, CRSP, Med, SMCC, or NAT.

127. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of TRAP, DRIP, ARC, CRSP, Med, SMCC, or NAT is chosen from the group consisting of TRAP240/DRIP250, TRAP230/DRIP240, DRIP205/CRSP200/TRIP2/PBP- /RB18A/TRAP220, hRGR1/CRSP150/DRIP150/TRAP170, TRAP150, CRSP130/hSur-2/DRIP130, TIG-1,; CRSP100/TRAP100/DRIP100, DRIP97, DRIP92/TRAP95, CRSP85, CRSP77/DRIP77/TRAP80, CRSP70/DRIP70, Ring3, hSRB10/hCDK8, DRIP36/hMEDp34, CRSP34, CRSP33/hmE7, hMED6, hSRB11/hCyclin C, hSOH1, hSRB7, is a protein of the androgen receptor complex, ANPK, ARIP3, PIAS family, PIASalpha, PIASbeta, PIASgamma, ARIP4, is a transcriptional co-repressor, N-CoR family, SMRT family, NCOR2/SMRT/TRAC1/CTG26/TNRC14/SMRTE, REA, MSin3, HDAC family, HDAC5, bHLH, suUSF, AP4, E-protein, E2A/E12, E47, HEB/ME1, HEB2/ME2/MITF-2A,B,C/SEF-2/TFE/TF4/R8f, TFE family, TFE3, TFEB, Myc family, Max family, Mad families, and WBSCR14.

128. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of neurogenins, Neurogenin-1/MATH4c, Neurogenin-2/MATH4a, Neurogenin-3/MATH4b, NeuroD, NeuroD-1, NeuroD-2,

NeuroD-3(6)/my051/NEX1/MATH2/Dlx-3, NeuroD-4/ATH-3/NeuroM), ATH, ATH-1/MATH1, ATH-5/MATH5, ASH, ASH-1/MASH1, ASH-2/LASH2, ASCL-3/reserved, NSCL, NSCL1/HEN1, NSCL2/HEN2, HAND, Hand1/eHAND/Thing-1, Hand2/dHAND/Thing-2, Mesencephalon-Olfactory Neuronal bHLHs, COE proteins, COE1, COE2/Olf-1/EBF-LIKE3, COE3/Olf-1, Homol/Mmot1, glia enriched bHLHs, OLIG proteins, Olig1, Olig2/protein kinase C-binding protein RACK17, Olig3, bHLH family of negative regulators, Ids, Id1, Id2, Id3, Id4, DIP1, HES, HES1, HES2, HES3, HES4, HES5, HES6, HES7, SHARP, SHARP1/DEC-2/eip1/Stra13, SHARP2/DEC-1/TR00067497_p, Hey/HRT proteins, Hey1/HRT1/HERP-2/HESR-2, Hey2/HRT2/HERP-1, HRT3, Lyl family, Lyl-1, Lyl-2, RGS family, RGS1, RGSRGS2/G0S8, RGS3/RGP3, capsulin, CENP-B, Mist1; Nhlh1, MOP3, Scleraxis, TCF15, bA305P22.3, Ipf-1/Pdx-1/Idx-1/Stf-1/Iuf-1/Gsf, beta.-catenin, GSK3, Groucho proteins, Groucho-1, Groucho-2, Groucho-3, Groucho-3, TCF family, TCF1A, B, C, D, E, F, G/LEF-1, TCF3, and TCF4, PC4, MBF1, Delta family, Serrate family, Jagged family, Dll1, Dll3, Dll4, Jagged1, Jagged2, Serrate2, Notch family, Notch1, Notch2, Notch3, Notch4, TAN-1, Bearded family, E(spl)m.alpha., E(spl)m2, E(spl)m4, E(spl)m6, Fringe family, Mfng, Rfng, Lfng, Deltex/dx-1, MAML1, RBP-Jk/CBF1/Su(H)/KBF2, RUNX, Chordin, Noggin, Follistatin, SMAD proteins, SMAD1, SMAD2, SMAD3, SMAD4, SAMD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10, SHH, IHH, Su(fu), GLI family, GLI/GLI1, Gli2, Gli3, Zic family, Zic/Zic1, Zic2, and Zic3.

129. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of Wing helix/forkhead

family of transcription factors, BF proteins, BF1, BF-2/Freac4, Fkh5/Foxb1/HFH-e5.1/Mf3, Fkh6/Freac7, HMG transcription factors, Sox proteins, Sox1, Sox2, Sox3, Sox4, Sox6, Sox10, Sox11, Sox13, Sox14 Sox18, Sox21, Sox22, Sox30, HMGIX, HMGIC, HMGIY, HMG-17, Hox proteins, Evx family, Evx1, Evx2, Mox family, Mox1, Mox2, NKL family, NK1, NK3, Nkx3.1, NK4, Lbx family, Lbx1, Lbx2, Tlx family, Tlx1, Tlx2, Tlx3, Emx/Ems family, Emx1, Emx2, Vax family, Vax1, Vax2, Hmx family, Hmx1, Hmx2, Hmx3, NK6 family, Nkx6.1, Msx/Msh family, Msx-1, Msx-2, Cdx, Cdx1, Cdx2, Xlox family, Lox3, Gsx family, Goosecoid, GSX, GSCL, En family, En-1, En-2, HB9 family, Hb9/HLXB9, Gbx family, Gbx1, Gbx2, Dbx family, Dbx-1, Dbx-2, Dll family, Dlx-1, Dlx-2, Dlx-4, Dlx-5, Dlx-7, Iroquois family, Xiro1, Irx2, Irx3, Irx4, Irx5, Irx6, Nkx, Nkx2.1/TTF-1, Nkx2.2/TTF-2, Nkx2.8, Nkx2.9, Nkx5.1, Nkx5.2, PBC family, Pbx1a, Pbx1b, Pbx2, Pbx3, Prd family, Otx-1, Otx-2, Phox2a, Phox2B, Ptx family, Pitx2, Pitx3/Ptx3, XANF family, Hesx1/XANF-1, BarH family, BarH, Brx2, Cut, Gtx, POU domain factor proteins, Brn2/XlPou2, Brn3a, Brn3b, Brn4/POU3F4, and Brn5/Pou6F1.

130. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factors is a member of the group consisting of transcription factors with a homeodomain region plus a LIM region, Isl1, Lhx2, Lhx3, Lhx4, Lhx5, Lhx6, Lhx7, Lhx9, LMO family, LMO1, LMO2, and LMO4.

131. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of Paired box transcription factors, Pax2, Pax3, Pax5, Pax6, Pax7, and Pax8, GATA family, Gata1, Gata2, Gata3, Gata4/5,

Gata6, MyT family, MyT1, MyT1l, MyT2, MyT3, SAL family HSal1, Sal2, Sall3, REST/NRSF/XBR, Snail family, Scratch/Scrt, Zf289, FLJ22251, MOZ, ZFP-38/RU49, Pzf, Mtsh1/teashirt, MTG8/CBF1A-homolog, TIS11D/BRF2/ERF2, TTF-I interacting peptide 21, Znf-HX, Zhx1, KOX1/NGO-St-66, ZFP-15/ZN-15, ZnF20, ZFP200, ZNF/282, HUB1, Finb/RREB1, Nuclear Receptors, liganded, ER family, TR family, RAR familiy, RXR family, PML-RAR family, PML-RXR family, Not1/Nurr, ROR, COUP-TF family, COUP-TF1, COUP-TF2, RING finger transcription factor proteins, KIAA0708, Bfp/ZNF179, BRAP2, KIAA0675, LUN,NSPc1, Neuralized family, neu/Neur-1, Neur-2, Neur-3, Neur-4, RING1A, SSA1/RO52, ZNF173, PIAS family, PIAS-alpha, PIAS-beta, PIAS-gamma, parkin family, and ZNF127 family.

132. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of proteins relating to cell-cycle progression-dedicated components that are part of the RNA polymerase II transcription complex, E2F family, E2F-1, E2F-3, E2F-4, E2F-5, DP family, DP-1, DP-2, p53 family, p53, p63, p73, mdm2; ATM, RB family, RB, p107, and p130.

133. (Previously Presented) The diagnostic device of Claim 111, wherein at least one transcription modulation factor is a member of the group consisting of factors involved in splicing.

134. (Previously Presented) The method of Claim 133, wherein at least one of the factors involved in splicing is chosen from the group consisting of Hu family, HuA, HuB, HuC, HuD, Musashi1, Nova family, Nova1, Nova2, SR proteins, B1C8, B4A11, ASF SRp20, SRp30, SRp40, SRp55, SRp75, SRm160, SRm300, CC1.3/CC1.4, Def-3/RBM6, SIAHBP/PUF60, Sip1, C1QBP/GC1Q-R/HABP1/P32, Staufen, TRIP, Zfr, CPSF, and Inducible poly(A)-Binding Protein (U33818).